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Endogenous florendoviruses shed new light on the taxonomy and evolution of *Caulimoviridae* and on plant-virus interactions

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Endogenous viral elements (EVEs) are molecular fossils that provide access to ancient viral sequences. As such, they are of great interest to unravel the evolution of viruses and refine their phylogeny [1]. In plants, most EVEs originate from viruses with DNA genomes in the families *Caulimoviridae* and *Geminiviridae* [2]. Representative genomes of a new genus of the *Caulimoviridae* were assembled from fragments of viral sequence that have been captured and preserved in the genome of a remarkable diversity of flowering plants ranging from ANITA-grade to monocots and dicots. Of the 76 reconstructed viral genomes, 34 represented distinct species that group into a new genus tentatively named 'Florendovirus', whose members seem to be extinct [3].

Endogenous florendovirus sequences have colonized the genomes of a large diversity of angiosperms, including important crops such as rice, cotton, soybean, maize, peach, strawberry, potato and tomato. In *Amborella trichopoda*, *Jatropha curcas*, *Vitis vinifera*, *Ricinus communis* and *Citrus* genomes, endogenous florendoviruses are present at a scale similar to that of some high copy number families of transposable elements, representing up to 1.3% of total genome content. Based on comparative phylogenies, integration events have been dated to 1.8-2.3 MYA in rice, but phylogeographic evidence points to an even older age of 20–34 MYA for this virus group. Conservation of endogenous florendovirus sequences over such long periods of time raises questions about their potential functions in plants.

In *V. vinifera*, *Oryza sativa* and *Sorghum bicolor*, molecular evidence point to a bipartite genome organization for some florendoviruses, a unique characteristic among viral retroelements. Considering that there are no examples of divided genomes in extant members of the *Caulimoviridae*, bipartite florendovirus genomes may therefore represent unsuccessful attempts in the evolution process of viral retroelements.

Mot-clés : *Caulimoviridae*; endogenous; *Florendovirus*; taxonomy; evolution; genome invasion.

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